



SEQUENCE LISTING



<110> Taupier, Raymond
Padigaru, Muralidhara
Rastelli, Luca
Spaderna, Steven
Shimkets, Richard
Zerhusen, Bryan
Spytek, Kimberly
Shenoy, Suresh
Li, Li
Gusev, Vladimir
Grosse, William
Alsobrook, John
Lepley, Denise
Burgess, Catherine
Gerlach, Valerie
Ellerman, Karen
MacDougall, John
Stone, David
Smithson, Glennda

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Glu Pro Glu Asp Val Tyr Ile Val Lys Asn Lys Pro Val Leu Leu Val
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Cys Lys Ala Val Pro Ala Thr Gln Ile Phe Phe Lys Cys Asn Gly Glu
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Trp Val Arg Gln Val Asp His Val Ile Glu Arg Ser Thr Asp Gly Ser
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Ser Gly Leu Pro Thr Met Glu Val Arg Ile Asn Val Ser Arg Gln Gln
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Val Glu Lys Val Phe Gly Leu Glu Glu Tyr Trp Cys Gln Cys Val Ala
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210 215 220

Asn Ile Val Ala Arg Arg Arg Ser Ala Ser Ala Ala Val Ile Val Tyr
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Gln Cys Leu Lys Asp Arg Ser Asn Phe Arg Phe Phe Gln Val Ser Lys
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Ser Asn Leu Phe Ser Lys Glu Asn Ala Leu Ile Ala Lys Lys Glu Met
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Leu Gln Gln Ile Phe Asn Thr Phe Ser Leu Asn Val Ser Gln Ser Phe
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Trp Asn Glu Ser Ser Leu Glu Arg Phe Leu Ser Arg Leu Tyr Gln Gln
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Ile Glu Lys Thr Glu Val Cys Leu Glu Gln Glu Thr Arg Lys Glu Gly
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Arg Ser Leu Leu Gln Arg Gly Asn Thr Ile Phe Arg Leu Lys Asn Tyr
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Glu Leu Asp Gly Val Gly Val Ser Ile Gly Ser Ala Ile His Thr Gln
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740	745	750
Arg Glu Glu Val Thr Gln Arg Ile Ala Thr Cys Gln Pro Leu Ser Gly		
755	760	765
Ala Leu Asp Asn Ser Arg Val Ile Leu Cys Asp Met Met Ala Asp Pro		
770	775	780
Trp Asn Ala Phe Trp Phe Cys Leu Ala Trp Cys Thr Phe Phe Leu Ile		
785	790	795
Pro Ser Ile Ile Phe Ala Val Lys Thr Ser Lys Tyr Phe Arg Pro Ile		
805	810	815
Arg Lys Arg Leu Ser Ser Thr Ser Ser Glu Glu Thr Gln Leu Phe His		
820	825	830
Ile Pro Arg Val Thr Ser Leu Lys Leu		
835	840	

<210> 7
 <211> 3261
 <212> DNA
 <213> Homo sapiens

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 cccactgccc ggcttgcctt ctgctgctgc cgctgccacc ggcgcgtgcgg gggacgagtg 420
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<210> 8
 <211> 841
 <212> PRT
 <213> Homo sapiens

<400> 8
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Gly Leu Ala Leu Ser Gln Leu Ala Ala Gly Ala Thr Asp Cys Lys Phe
 20 25 30

Leu Gly Pro Ala Glu His Leu Thr Phe Thr Pro Ala Ala Arg Ala Arg
 35 40 45

Trp Leu Ala Pro Arg Val Arg Ala Pro Gly Leu Leu Asp Ser Leu Tyr
 50 55 60

Gly Thr Val Arg Arg Phe Leu Ser Val Val Gln Leu Asn Pro Phe Pro
 65 70 75 80

Ser Glu Leu Val Lys Ala Leu Leu Asn Glu Leu Ala Ser Val Lys Val
 85 90 95

Asn Glu Val Val Arg Tyr Glu Ala Gly Tyr Val Val Cys Ala Val Ile
 100 105 110

Ala Gly Leu Tyr Leu Leu Val Pro Thr Ala Gly Leu Cys Phe Cys
 115 120 125

Cys Cys Arg Cys His Arg Arg Cys Gly Gly Arg Val Lys Thr Glu His
 130 135 140

Lys Ala Leu Ala Cys Glu Arg Ala Ala Leu Met Val Phe Leu Leu Leu
 145 150 155 160

Thr Thr Leu Leu Leu Ile Gly Val Val Cys Ala Phe Val Thr Asn
 165 170 175
 Gln Arg Thr His Glu Gln Met Gly Pro Ser Ile Glu Ala Met Pro Glu
 180 185 190
 Thr Leu Leu Ser Leu Trp Gly Leu Val Ser Asp Val Pro Gln Glu Leu
 195 200 205
 Gln Ala Val Ala Gln Gln Phe Ser Leu Pro Gln Glu Gln Val Ser Glu
 210 215 220
 Glu Leu Asp Gly Val Gly Val Ser Ile Gly Ser Ala Ile His Thr Gln
 225 230 235 240
 Leu Arg Ser Ser Val Tyr Pro Leu Leu Ala Ala Val Gly Ser Leu Gly
 245 250 255
 Gln Val Leu Gln Val Ser Val His His Leu Gln Thr Leu Asn Ala Thr
 260 265 270
 Val Val Glu Leu Gln Ala Gly Gln Gln Asp Leu Glu Pro Ala Ile Arg
 275 280 285
 Glu His Arg Asp Arg Leu Leu Glu Leu Leu Gln Glu Ala Arg Cys Gln
 290 295 300
 Gly Asp Cys Ala Gly Ala Leu Ser Trp Ala Arg Thr Leu Glu Leu Gly
 305 310 315 320
 Ala Asp Phe Ser Gln Val Pro Ser Val Asp His Val Leu His Gln Leu
 325 330 335
 Lys Gly Val Pro Glu Ala Asn Phe Ser Ser Met Val Gln Glu Glu Asn
 340 345 350
 Ser Thr Phe Asn Ala Leu Pro Ala Leu Ala Ala Met Gln Thr Ser Ser
 355 360 365
 Val Val Gln Glu Leu Lys Lys Ala Val Ala Gln Gln Pro Glu Gly Val
 370 375 380
 Arg Thr Leu Ala Glu Gly Phe Pro Gly Leu Glu Ala Ala Ser Arg Trp
 385 390 395 400
 Ala Gln Ala Leu Gln Glu Val Glu Glu Ser Ser Arg Pro Tyr Leu Gln
 405 410 415
 Glu Val Gln Arg Tyr Glu Thr Tyr Arg Trp Ile Val Gly Cys Val Leu
 420 425 430
 Cys Ser Val Val Leu Phe Val Val Leu Cys Asn Leu Leu Gly Leu Asn
 435 440 445
 Leu Gly Ile Trp Gly Leu Ser Ala Arg Asp Asp Pro Ser His Pro Glu
 450 455 460
 Ala Lys Gly Glu Ala Gly Ala Arg Phe Leu Met Ala Gly Val Gly Leu
 465 470 475 480
 Ser Phe Leu Phe Ala Ala Pro Leu Ile Leu Leu Val Phe Ala Thr Phe
 485 490 495

Leu Val Gly Gly Asn Val Gln Thr Leu Val Cys Gln Ser Trp Glu Asn
 500 505 510
 Gly Glu Leu Phe Glu Phe Ala Asp Thr Pro Gly Asn Leu Pro Pro Ser
 515 520 525
 Met Asn Leu Ser Gln Leu Leu Gly Leu Arg Lys Asn Ile Ser Ile His
 530 535 540
 Gln Ala Tyr Gln Gln Cys Lys Glu Gly Ala Ala Leu Trp Thr Val Leu
 545 550 555 560
 Gln Leu Asn Asp Ser Tyr Asp Leu Glu Glu His Leu Asp Ile Asn Gln
 565 570 575
 Tyr Thr Asn Lys Leu Arg Gln Glu Leu Gln Ser Leu Lys Val Asp Thr
 580 585 590
 Gln Ser Leu Asp Leu Leu Ser Ser Ala Ala Arg Arg Asp Leu Glu Ala
 595 600 605
 Leu Gln Ser Ser Gly Leu Gln Arg Ile His Tyr Pro Asp Phe Leu Val
 610 615 620
 Gln Ile Gln Arg Pro Val Val Lys Thr Ser Met Glu Gln Leu Ala Gln
 625 630 635 640
 Glu Leu Gln Gly Leu Ala Gln Ala Gln Asp Asn Ser Val Leu Gly Gln
 645 650 655
 Arg Leu Gln Glu Glu Ala Gln Gly Leu Arg Asn Leu His Gln Glu Lys
 660 665 670
 Val Val Pro Gln Gln Ser Leu Val Ala Lys Leu Asn Leu Ser Val Arg
 675 680 685
 Ala Leu Glu Ser Ser Ala Pro Asn Leu Gln Val Ala Ala Val Gly Gly
 690 695 700
 Asp Leu Glu Thr Ser Asp Val Leu Ala Asn Val Thr Tyr Leu Lys Gly
 705 710 715 720
 Glu Leu Pro Ala Trp Ala Ala Arg Ile Leu Arg Asn Val Ser Glu Cys
 725 730 735
 Phe Leu Ala Arg Glu Met Gly Tyr Phe Ser Gln Tyr Val Ala Trp Val
 740 745 750
 Arg Glu Glu Val Thr Gln Arg Ile Ala Thr Cys Gln Pro Leu Ser Gly
 755 760 765
 Ala Leu Asp Asn Ser Arg Val Ile Leu Cys Asp Met Met Ala Asp Pro
 770 775 780
 Trp Asn Ala Phe Trp Phe Cys Leu Ala Trp Cys Thr Phe Phe Leu Ile
 785 790 795 800
 Pro Ser Ile Ile Phe Ala Val Lys Thr Ser Lys Tyr Phe Arg Pro Ile
 805 810 815
 Arg Lys Arg Leu Ser Ser Thr Ser Ser Glu Glu Thr Gln Leu Phe His
 820 825 830
 Ile Pro Arg Val Thr Ser Leu Lys Leu

835

840

<210> 9
<211> 2007
<212> DNA
<213> Homo sapiens

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actctggaga catgtctgca acatcaatgc tgccttttgc tggccatca acatcttc 1980
ctggggctat tttgcgtat tccacag 2007

<210> 10
<211> 664
<212> PRT
<213> Homo sapiens

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His Ile Ala Leu Asp Ser Arg Val Gly Leu His Ala Tyr Asp Ile Ser
20 25 30

Val Val Val Ile Tyr Phe Val Phe Val Ile Ala Val Gly Ile Trp Ser
35 40 45

Ser Ile Arg Ala Ser Arg Gly Thr Ile Gly Gly Tyr Phe Leu Ala Gly
50 55 60

Arg Ser Met Ser Trp Trp Pro Val Ile Gly Ala Ser Leu Met Ser Ser

65	70	75	80
Asn Val Gly Ser Gly Leu Phe Ile Gly Leu Ala Gly Thr Gly Ala Ala			
85	90	95	
Gly Gly Leu Ala Val Gly Gly Phe Glu Trp Asn Ala Thr Trp Leu Leu			
100	105	110	
Leu Ala Leu Gly Trp Val Phe Val Pro Val Tyr Ile Ala Ala Gly Val			
115	120	125	
Val Thr Met Pro Gln Tyr Leu Lys Lys Arg Phe Gly Gly Gln Arg Ile			
130	135	140	
Gln Met Tyr Met Ser Val Leu Ser Leu Ile Leu Tyr Ile Phe Thr Lys			
145	150	155	160
Ile Ser Val Asp Ile Phe Ser Gly Ala Leu Phe Ile Gln Met Ala Leu			
165	170	175	
Gly Trp Asn Leu Tyr Leu Ser Thr Gly Ile Leu Leu Val Val Thr Ala			
180	185	190	
Val Tyr Thr Ile Ala Gly Gly Leu Met Ala Val Ile Tyr Thr Asp			
195	200	205	
Ala Leu Gln Thr Val Ile Met Val Gly Gly Ala Leu Val Leu Met Phe			
210	215	220	
Leu Gly Lys Glu Glu Thr Gly Trp Tyr Pro Gly Leu Glu Gln Arg Tyr			
225	230	235	240
Arg Gln Ala Ile Pro Asn Val Thr Val Pro Asn Thr Thr Cys His Leu			
245	250	255	
Pro Arg Pro Asp Ala Phe His Met Leu Arg Asp Pro Val Ser Gly Asp			
260	265	270	
Ile Pro Trp Pro Gly Leu Ile Phe Gly Leu Thr Val Leu Ala Thr Trp			
275	280	285	
Cys Trp Cys Thr Asp Gln Val Ile Val Gln Arg Ser Leu Ser Ala Lys			
290	295	300	
Ser Leu Ser His Ala Lys Gly Gly Ser Val Leu Gly Gly Tyr Leu Lys			
305	310	315	320
Ile Leu Pro Met Phe Phe Ile Val Met Pro Gly Met Ile Ser Arg Ala			
325	330	335	
Leu Phe Pro Glu Ile Ala Cys Met Cys Val Pro Val Cys Thr His Ala			
340	345	350	
Cys Ala Ala Arg Lys Arg Lys Glu Gly Val Leu Gln Gly Leu Val Val			
355	360	365	
Ala Val Arg Leu Ser Pro Gly Leu Arg Gly Leu Met Ile Ala Val Ile			
370	375	380	
Met Ala Ala Leu Met Ser Ser Leu Thr Ser Ile Phe Asn Ser Ser Ser			
385	390	395	400
Thr Leu Phe Thr Ile Asp Val Trp Gln Arg Phe Arg Arg Lys Ser Thr			
405	410	415	

Glu Gln Glu Leu Met Val Val Gly Arg Val Phe Val Val Phe Leu Val
 420 425 430
 Val Ile Ser Ile Leu Trp Ile Pro Ile Ile Gln Ser Ser Asn Ser Gly
 435 440 445
 Gln Leu Phe Asp Tyr Ile Gln Ala Val Thr Ser Tyr Leu Ala Pro Pro
 450 455 460
 Ile Thr Ala Leu Phe Leu Leu Ala Ile Phe Cys Lys Arg Val Thr Glu
 465 470 475 480
 Gln Gly Ala Phe Trp Gly Leu Val Phe Gly Leu Gly Val Gly Leu Leu
 485 490 495
 Arg Met Ile Leu Glu Phe Ser Tyr Pro Ala Pro Ala Cys Gly Glu Val
 500 505 510
 Asp Arg Arg Pro Ala Val Leu Lys Asp Phe His Tyr Leu Tyr Phe Ala
 515 520 525
 Ile Leu Leu Cys Gly Leu Thr Ala Ile Val Ile Val Ile Val Ser Leu
 530 535 540
 Cys Thr Thr Pro Ile Pro Glu Leu His Thr Tyr Ile Tyr Cys Gly Thr
 545 550 555 560
 Ile His Asn Ser Lys Asp Phe Glu Pro Ile Gln Ile Ser Asn Asn Glu
 565 570 575
 Gln Ala Leu Ser Pro Ala Glu Lys Ala Ala Leu Glu Gln Lys Leu Thr
 580 585 590
 Ser Ile Glu Glu Glu Ser Ser Gly Phe Val Pro Pro Ala Trp Ser Trp
 595 600 605
 Phe Cys Gly Leu Ser Gly Thr Pro Glu Gln Ala Leu Ser Pro Ala Glu
 610 615 620
 Lys Ala Ala Leu Glu Gln Lys Leu Thr Ser Ile Glu Glu Glu Pro Leu
 625 630 635 640
 Trp Arg His Val Cys Asn Ile Asn Ala Val Leu Leu Leu Ala Ile Asn
 645 650 655
 Ile Phe Leu Trp Gly Tyr Phe Ala
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<210> 11
 <211> 2153
 <212> DNA
 <213> Homo sapiens

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 gcatctaacg cttggtttgc tgctgcccag tcagagccag aggaaggat atctgtttt 180
 gaactggatt atgactatgt gcaaattcct tatgaggtca ctctctggat acttctagca 240
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 aagctgcccac cctggctgtt cctttgggtt aggttcggtc gaggtggaca gctgaccatg 2100
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<210> 12
 <211> 717
 <212> PRT
 <213> Homo sapiens

<400> 12
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Leu Leu Val Ala Leu Glu Cys Ser Glu Ala Ser Ser Asp Leu Asn Glu
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Ser Ala Asn Ser Thr Ala Gln Tyr Ala Ser Asn Ala Trp Phe Ala Ala
 35 40 45

Ala Ser Ser Glu Pro Glu Glu Gly Ile Ser Val Phe Glu Leu Asp Tyr
 50 55 60

Asp Tyr Val Gln Ile Pro Tyr Glu Val Thr Leu Trp Ile Leu Leu Ala
 65 70 75 80

Ser Leu Ala Lys Ile Gly Phe His Leu Tyr His Arg Leu Pro Gly Leu
 85 90 95

Met Pro Glu Ser Cys Leu Leu Ile Leu Val Gly Ala Leu Val Gly Gly
 100 105 110

Ile Ile Phe Gly Thr Asp His Lys Ser Pro Pro Val Met Asp Ser Ser
 115 120 125

Ile Tyr Phe Leu Tyr Leu Leu Pro Pro Ile Val Leu Glu Gly Gly Tyr
 130 135 140

Phe Met Pro Thr Arg Pro Phe Phe Glu Asn Ile Gly Ser Ile Leu Trp

145	150	155	160
Trp Ala Val Leu Gly Ala Leu Ile Asn Ala Leu Gly Ile Gly Leu Ser			
165	170	175	
Leu Tyr Leu Ile Cys Gln Val Lys Ala Phe Gly Leu Gly Asp Val Asn			
180	185	190	
Leu Leu Gln Asn Leu Leu Phe Gly Ser Leu Ile Ser Ala Val Asp Pro			
195	200	205	
Val Ala Val Leu Ala Val Phe Glu Glu Ala Arg Val Asn Glu Gln Leu			
210	215	220	
Tyr Met Met Ile Phe Gly Glu Ala Leu Leu Asn Asp Gly Ile Thr Val			
225	230	235	240
Val Leu Tyr Asn Met Leu Ile Ala Phe Thr Lys Met His Lys Phe Glu			
245	250	255	
Asp Ile Glu Thr Val Asp Ile Leu Ala Gly Cys Ala Arg Phe Ile Val			
260	265	270	
Val Gly Leu Gly Gly Val Leu Phe Gly Ile Val Phe Gly Phe Ile Ser			
275	280	285	
Ala Phe Ile Thr Arg Phe Thr Gln Asn Ile Ser Ala Ile Glu Pro Leu			
290	295	300	
Ile Val Phe Met Phe Ser Tyr Leu Ser Tyr Leu Ala Ala Glu Thr Leu			
305	310	315	320
Tyr Leu Ser Gly Ile Leu Ala Ile Thr Ala Cys Ala Val Thr Met Lys			
325	330	335	
Lys Tyr Val Glu Glu Asn Val Ser Gln Thr Ser Tyr Thr Ile Lys			
340	345	350	
Tyr Phe Met Lys Met Leu Ser Ser Val Ser Glu Thr Leu Ile Phe Ile			
355	360	365	
Phe Met Gly Val Ser Thr Val Gly Lys Asn His Glu Trp Asn Trp Ala			
370	375	380	
Phe Ile Cys Phe Thr Leu Ala Phe Cys Gln Ile Trp Arg Ala Ile Ser			
385	390	395	400
Val Phe Ala Leu Phe Tyr Ile Ser Asn Gln Phe Arg Thr Phe Pro Phe			
405	410	415	
Ser Ile Lys Asp Gln Cys Ile Ile Phe Tyr Ser Gly Val Arg Gly Ala			
420	425	430	
Gly Ser Phe Ser Leu Ala Phe Leu Leu Pro Leu Ser Leu Phe Pro Arg			
435	440	445	
Lys Lys Met Phe Val Thr Ala Thr Leu Val Val Ile Tyr Phe Thr Val			
450	455	460	
Phe Ile Gln Gly Ile Thr Val Gly Pro Leu Val Arg Tyr Leu Asp Val			
465	470	475	480
Lys Lys Thr Asn Lys Lys Glu Ser Ile Asn Glu Glu Leu His Ile Arg			
485	490	495	

Leu Met Asp His Leu Lys Ala Gly Ile Glu Asp Val Cys Gly His Trp
 500 505 510
 Ser His Tyr Gln Val Arg Asp Lys Phe Lys Lys Phe Asp His Arg Tyr
 515 520 525
 Leu Arg Lys Ile Leu Ile Arg Lys Asn Leu Pro Lys Ser Ser Ile Val
 530 535 540
 Ser Leu Tyr Lys Lys Leu Glu Met Lys Gln Ala Ile Glu Met Val Glu
 545 550 555 560
 Thr Gly Ile Leu Ser Ser Thr Ala Phe Ser Ile Pro His Gln Ala Gln
 565 570 575
 Arg Ile Gln Gly Ile Lys Arg Leu Ser Pro Glu Asp Val Glu Ser Ile
 580 585 590
 Arg Asp Ile Leu Thr Ser Asn Met Tyr Gln Val Arg Gln Arg Thr Leu
 595 600 605
 Ser Tyr Asn Lys Tyr Asn Leu Lys Pro Gln Thr Ser Glu Lys Gln Ala
 610 615 620
 Lys Glu Ile Leu Ile Arg Arg Gln Asn Thr Leu Arg Glu Ser Met Arg
 625 630 635 640
 Lys Gly His Ser Leu Pro Trp Gly Lys Pro Ala Gly Thr Lys Asn Ile
 645 650 655
 Arg Tyr Leu Ser Tyr Pro Tyr Gly Asn Pro Gln Ser Ala Gly Arg Asp
 660 665 670
 Thr Arg Ala Ala Gly Phe Ser Gly Lys Leu Pro Thr Trp Leu Leu Leu
 675 680 685
 Trp Leu Arg Phe Gly Arg Gly Gln Leu Thr Met Asp Thr Ala Gly
 690 695 700
 Thr Ile Thr Gly Pro Ile Val Leu Cys Ser Lys Lys Asn
 705 710 715

<210> 13
 <211> 251
 <212> DNA
 <213> Homo sapiens

<400> 13
 gacaggattc cacagcttg cactcctggc tctgctttct ctgcaaccat gtctgacaaa 60
 cccagcatgg ctgagattga gacactcaat aagcagagat tgaagaaggc agaaaacacaa 120
 gagataaaatc caccgccttc aagagaaaaca aacgaaaagaa gcaaacaggt gaattataat 180
 gagctgtgag ctgcgaatag gtactgcaca ttccatgggc attgccttct tattttactt 240
 cttagctg t 251

<210> 14
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ser Asp Lys Pro Ser Met Ala Glu Ile Glu Thr Leu Asn Lys Gln

1	5	10	15												
Arg	Leu	Lys	Lys	Ala	Glu	Thr	Gln	Glu	Ile	Asn	Pro	Pro	Pro	Ser	Arg
20								25						30	
Glu	Thr	Asn	Glu	Arg	Ser	Lys	Gln	Val	Asn	Tyr	Asn	Glu	Leu		
35								40						45	

<210> 15
 <211> 2144
 <212> DNA
 <213> Homo sapiens

<400> 15
 atgcttcaca cggccatatac atgctggca g ccattcctgg gtctggctgt ggtgttaatc 60
 ttcatggat ccaccattgg ctgccccgt cgctgtgagt gctctgcca gaacaatct 120
 gttagctgtc acagaaggcg attgatcgcc atcccagagg gcattcccat cgaacacaaa 180
 atcttggacc tcagtaaaaa caggctaaaa agcgtaacc ctgaagaatt catacatat 240
 cctctgctgg aagagataga cttgagtgac aacatcattg ccaatgtgga accaggagca 300
 ttcaacaatc tcttaaacct gcgttccctc cgcctaaaag gcaatcgct aaagctggtc 360
 ccttgggag tattcacggg gctgtccaaat ctcactaagc ttgacattag tgagaataag 420
 attgtcattt tactagacta catgttccaa gatctacata acctgaagt tctagaagt 480
 ggggacaatg atttggttta tatatcacac agggcattca gtgggcttct tagcttggag 540
 cagctcaccc tggagaaaatg caacttaaca gcagtaccaa cagaagccct ctcccacctc 600
 cgcagcctca tcagcctgca tctgaagcat ctcaatatca acaatatgcc tgtgtatgcc 660
 tttaaaagat tgttccaccc gaaacaccta gagattgact attggcctt actgatatg 720
 atgcctgcca atagccctca cggtctcaac ctcacatccc tttcagtcac caacaccaat 780
 ctgtctactg tacccttc tgcctttaaa cacctggat acctgactca ccttaacctc 840
 tcctacaatc ccatcagcac tattgaagca ggcatgttct ctgacccgtat ccgccttcag 900
 gagcttcata tagtggggc ccaagcttcg accatggc tcactccctt ccaaggcgtc 960
 cgcttcatac gcgtgcctaa tttgtctca g aacctgtgg aacttttgg a agagaatgtc 1020
 ttctccccc ctagggtctt ggaggtctt agcattaaaca acaaccctt ggcctgtgac 1080
 tgccgccttc tctggatctt gcagcagac cccacccgtc agtttgggg ccagcaacct 1140
 atgtgtctg gcccagacac catccgtgag aggtcttca aggatttca tagactgccc 1200
 ctttctttt actttaccc caaaaaaaaacc aaaaatccgtg aaaaagaattt gcagcatctg 1260
 ctagtagatg aagggcagac agtccagcta gaatgcagt cagatggaga cccgcagcct 1320
 gtgatttcctt ggggtacacc cccaaggcgt ttcatcacca ccaagtccaa tggaaagagcc 1380
 accgtgttgg gtgatggcac cttggaaatc cgcttgc cccaggatcaaga cagccggatg 1440
 tatgtttgca tcgcttagaa tgctgtggg aatgatactt tcacagccctc cttactgtg 1500
 aaaggattcg cttcagatcg tttctttat gcaacagga cccctatgtt catgaccgac 1560
 tccaatgaca ccatttccaa tggcagcaat gccaataactt tttccctgaa ccttaaaaca 1620
 atactgggtt ctacagctat gggctgcttc acattcctgg gagtgggtt attttgtttt 1680
 ctttccctt ttgtgtggag ccgaggaaa gcaagcaca aaaaacagcat tgacccttg 1740
 tatgtgccc aaaaaaaaaacc ttgtgtgtt gtggaaagggg aggttagctgg acccaggagg 1800
 ttcaacatga aaatgattt aaggcccacc cctcacatta ctgtctttt gtcaatgtgg 1860
 gtaatcagta agacagtatg gcacagtaaa ttactagatt aagaggcagc catgtgcagc 1920
 tgccctgttca tcaaaaggcag ggtctatgga agcaggagga cttccatgg agactctcca 1980
 tcgaaaggca ggcaggcagg catgtgtcag agcccttcac acagtggat actaagtgtt 2040
 tgcgttgcaa atattggcgt tctgggatc tcagtaatga acctgaatat ttggctcaca 2100
 ctcacggaca attattcagc attttctacc actgcaaaaaaaa 2144

<210> 16
 <211> 606
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Leu His Thr Ala Ile Ser Cys Trp Gln Pro Phe Leu Gly Leu Ala
 1 5 10 15
 Val Val Leu Ile Phe Met Gly Ser Thr Ile Gly Cys Pro Ala Arg Cys
 20 25 30

Glu Cys Ser Ala Gln Asn Lys Ser Val Ser Cys His Arg Arg Arg Leu
 35 40 45
 Ile Ala Ile Pro Glu Gly Ile Pro Ile Glu Thr Lys Ile Leu Asp Leu
 50 55 60
 Ser Lys Asn Arg Leu Lys Ser Val Asn Pro Glu Glu Phe Ile Ser Tyr
 65 70 75 80
 Pro Leu Leu Glu Glu Ile Asp Leu Ser Asp Asn Ile Ile Ala Asn Val
 85 90 95
 Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Ser Leu Arg Leu
 100 105 110
 Lys Gly Asn Arg Leu Lys Leu Val Pro Leu Gly Val Phe Thr Gly Leu
 115 120 125
 Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys Ile Val Ile Leu
 130 135 140
 Leu Asp Tyr Met Phe Gln Asp Leu His Asn Leu Lys Ser Leu Glu Val
 145 150 155 160
 Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu
 165 170 175
 Leu Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ala Val
 180 185 190
 Pro Thr Glu Ala Leu Ser His Leu Arg Ser Leu Ile Ser Leu His Leu
 195 200 205
 Lys His Leu Asn Ile Asn Asn Met Pro Val Tyr Ala Phe Lys Arg Leu
 210 215 220
 Phe His Leu Lys His Leu Glu Ile Asp Tyr Trp Pro Leu Leu Asp Met
 225 230 235 240
 Met Pro Ala Asn Ser Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Val
 245 250 255
 Thr Asn Thr Asn Leu Ser Thr Val Pro Phe Leu Ala Phe Lys His Leu
 260 265 270
 Val Tyr Leu Thr His Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile
 275 280 285
 Glu Ala Gly Met Phe Ser Asp Leu Ile Arg Leu Gln Glu Leu His Ile
 290 295 300
 Val Gly Ala Gln Leu Arg Thr Ile Glu Pro His Ser Phe Gln Gly Leu
 305 310 315 320
 Arg Phe Leu Arg Val Leu Asn Val Ser Gln Asn Leu Leu Glu Thr Leu
 325 330 335
 Glu Glu Asn Val Phe Ser Ser Pro Arg Ala Leu Glu Val Leu Ser Ile
 340 345 350
 Asn Asn Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Ile Leu Gln
 355 360 365

Arg Gln Pro Thr Leu Gln Phe Gly Gly Gln Gln Pro Met Cys Ala Gly
 370 375 380
 Pro Asp Thr Ile Arg Glu Arg Ser Phe Lys Asp Phe His Ser Thr Ala
 385 390 395 400
 Leu Ser Phe Tyr Phe Thr Cys Lys Lys Pro Lys Ile Arg Glu Lys Lys
 405 410 415
 Leu Gln His Leu Leu Val Asp Glu Gly Gln Thr Val Gln Leu Glu Cys
 420 425 430
 Ser Ala Asp Gly Asp Pro Gln Pro Val Ile Ser Trp Val Thr Pro Arg
 435 440 445
 Arg Arg Phe Ile Thr Thr Lys Ser Asn Gly Arg Ala Thr Val Leu Gly
 450 455 460
 Asp Gly Thr Leu Glu Ile Arg Phe Ala Gln Asp Gln Asp Ser Gly Met
 465 470 475 480
 Tyr Val Cys Ile Ala Ser Asn Ala Ala Gly Asn Asp Thr Phe Thr Ala
 485 490 495
 Ser Leu Thr Val Lys Gly Phe Ala Ser Asp Arg Phe Leu Tyr Ala Asn
 500 505 510
 Arg Thr Pro Met Tyr Met Thr Asp Ser Asn Asp Thr Ile Ser Asn Gly
 515 520 525
 Ser Asn Ala Asn Thr Phe Ser Leu Asp Leu Lys Thr Ile Leu Val Ser
 530 535 540
 Thr Ala Met Gly Cys Phe Thr Phe Leu Gly Val Val Leu Phe Cys Phe
 545 550 555 560
 Leu Leu Leu Phe Val Trp Ser Arg Gly Lys Gly Lys His Lys Asn Ser
 565 570 575
 Ile Asp Leu Glu Tyr Val Pro Lys Lys Asn His Gly Ala Val Val Glu
 580 585 590
 Gly Glu Val Ala Gly Pro Arg Arg Phe Asn Met Lys Met Ile
 595 600 605

<210> 17
 <211> 2187
 <212> DNA
 <213> Homo sapiens

<400> 17
 aatcatgagg aacctataac ccttttggcc acatgcaaaa aagcaagacc cgtgaccaag 60
 gttagacta agaagtggag tcatgcttca cacggccata tcatgctggc agccattcct 120
 gggctggct gtgggttaa tcttcatggg acccaccatt ggctgccccg ctcgctgtga 180
 gtgctctgcc cagaacaaat ctgtagctg tcacagaagg cgattgatcg ccatccccaga 240
 gggcattccc atcgaaacca aaatcttcaa cctcagtaaa aacaggctaa aaagcgtcaa 300
 ccctgaagaa ttcatatcat atccctctgct ggaagagata gacttgagtg acaacatcat 360
 tgccaatgtg gaaccaggag cattcaacaa tctcttaac ctgcgttccc tccgcctaaa 420
 aggcaatcgt ctaaagctgg tccctttggg agtattcacg gggctgtcca atctcactaa 480
 gcttgacatt agtgagaata agattgtcat tttactagac tacatgttcc aagatctaca 540
 taacctgaag tctctagaag tgggggacaa tgatttgggt tatatatcac acagggcatt 600
 cagtgggctt cttagcttgg agcagctcac cctggagaaa tgcaacttaa cagcagtacc 660
 aacagaagcc ctctccacc tccgcagcct catcagcctg catctgaagc atctcaatat 720

caacaatatg cctgtgtata cctttaaaag attgttccac ctgaaacacc tagagattga 780
 ctattggcct ttactggata ttagtgcctgc caatacgctc tacggctctca acctcacacc 840
 ccttcagtc accaacacca atctgtctac tgtacccttc cttgccttta aacacctggt 900
 atacctgact caccttaacc ttcctacaa tcccattcagc actattgaag caggcatgtt 960
 ctctgacctg atccgccttc aggagcttca tatagtgggg gcccagcttc gcaccattga 1020
 gcctcactcc ttccaaggc tcgccttc acgcgtgctc aatgtgtctc agaacctgct 1080
 ggaaactttg gaagagaatg tcttctccct cccttagggct ctggaggct tgagcattaa 1140
 caacaaccct ctggcctgtg actgcccct tctctggatc ttgcagcgcac agccaccct 1200
 gcagtttggt ggcgcagcaac ctatgtgtgc tggccagac accatccgtg agaggtctt 1260
 caaggatttc catagcaactg ccccttctt ttacttacc tgcaaaaaac ccaaataccg 1320
 tgaaaagaag ttgcagcatc tgtagtaga tgaagggcag acagtccagc tagaatgcag 1380
 tgcagatgga gaccgcgcagc ctgtgatttc ctgggtgaca ccccgaaaggc gtttcatcac 1440
 cacaagtcc aatggaaagag ccaccgtgtt gggatggc accttggaaa tccgccttc 1500
 ccaggatcaa gacagcggga ttagtgtttt catcgcttagc aatgtgtctg ggaatgatac 1560
 cttcacagcc tccttaactg tggaaaggatt cgcttcagat cgtttctt atgcgaacag 1620
 gaccctatg tacatgaccg actccaatga caccatttcc aatggcacca atgccaatac 1680
 ttttccctg gacctaaaaa caatactggt gtctcagct atgggctgt tcacattcct 1740
 gggagtgggtt ttatgggtt ttcttcctt ttttgggtt agccgagggaa aaggcaagca 1800
 caaaaacagc attgacccctt agtatgtgcc cagaaaaaac agtgggtctg ttgtggagg 1860
 ggaggttagct ggaccaggaa ggttcaacat gaaaatgatt tgaaggccca cccctcacat 1920
 tactgtctct ttgtcaatgt ggttaatcag taagacagta tggcacagata aattactaga 1980
 ttaagaggca gccatgtgca gctgcctctg tatcaaaaagc agggtctatg gaagcaggag 2040
 gacttccaat ggagactctc catcgaaagg caggcaggca gcatgtgtc agacccttc 2100
 acacagtggg atactaagtg ttgcgttgc aaatattggc gttctggga tctcagtaat 2160
 gaacctgaat attggctca cactcac 2187

<210> 18
 <211> 606
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Leu His Thr Ala Ile Ser Cys Trp Gln Pro Phe Leu Gly Leu Ala
 1 5 10 15

Val Val Leu Ile Phe Met Gly Pro Thr Ile Gly Cys Pro Ala Arg Cys
 20 25 30

Glu Cys Ser Ala Gln Asn Lys Ser Val Ser Cys His Arg Arg Arg Leu
 35 40 45

Ile Ala Ile Pro Glu Gly Ile Pro Ile Glu Thr Lys Ile Leu Asn Leu
 50 55 60

Ser Lys Asn Arg Leu Lys Ser Val Asn Pro Glu Glu Phe Ile Ser Tyr
 65 70 75 80

Pro Leu Leu Glu Glu Ile Asp Leu Ser Asp Asn Ile Ile Ala Asn Val
 85 90 95

Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Ser Leu Arg Leu
 100 105 110

Lys Gly Asn Arg Leu Lys Leu Val Pro Leu Gly Val Phe Thr Gly Leu
 115 120 125

Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys Ile Val Ile Leu
 130 135 140

Leu Asp Tyr Met Phe Gln Asp Leu His Asn Leu Lys Ser Leu Glu Val
 145 150 155 160

Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu

165	170	175	
Leu Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ala Val			
180	185	190	
Pro Thr Glu Ala Leu Ser His Leu Arg Ser Leu Ile Ser Leu His Leu			
195	200	205	
Lys His Leu Asn Ile Asn Asn Met Pro Val Tyr Thr Phe Lys Arg Leu			
210	215	220	
Phe His Leu Lys His Leu Glu Ile Asp Tyr Trp Pro Leu Leu Asp Met			
225	230	235	240
Met Pro Ala Asn Ser Leu Tyr Gly Leu Asn Leu Thr Pro Leu Ser Val			
245	250	255	
Thr Asn Thr Asn Leu Ser Thr Val Pro Phe Leu Ala Phe Lys His Leu			
260	265	270	
Val Tyr Leu Thr His Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile			
275	280	285	
Glu Ala Gly Met Phe Ser Asp Leu Ile Arg Leu Gln Glu Leu His Ile			
290	295	300	
Val Gly Ala Gln Leu Arg Thr Ile Glu Pro His Ser Phe Gln Gly Leu			
305	310	315	320
Arg Phe Leu Arg Val Leu Asn Val Ser Gln Asn Leu Leu Glu Thr Leu			
325	330	335	
Glu Glu Asn Val Phe Ser Ser Pro Arg Ala Leu Glu Val Leu Ser Ile			
340	345	350	
Asn Asn Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Ile Leu Gln			
355	360	365	
Arg Gln Pro Thr Leu Gln Phe Gly Gly Gln Pro Met Cys Ala Gly			
370	375	380	
Pro Asp Thr Ile Arg Glu Arg Ser Phe Lys Asp Phe His Ser Thr Ala			
385	390	395	400
Leu Ser Phe Tyr Phe Thr Cys Lys Lys Pro Lys Ile Arg Glu Lys Lys			
405	410	415	
Leu Gln His Leu Leu Val Asp Glu Gly Gln Thr Val Gln Leu Glu Cys			
420	425	430	
Ser Ala Asp Gly Asp Pro Gln Pro Val Ile Ser Trp Val Thr Pro Arg			
435	440	445	
Arg Arg Phe Ile Thr Thr Lys Ser Asn Gly Arg Ala Thr Val Leu Gly			
450	455	460	
Asp Gly Thr Leu Glu Ile Arg Phe Ala Gln Asp Gln Asp Ser Gly Met			
465	470	475	480
Tyr Val Cys Ile Ala Ser Asn Ala Ala Gly Asn Asp Thr Phe Thr Ala			
485	490	495	
Ser Leu Thr Val Lys Gly Phe Ala Ser Asp Arg Phe Leu Tyr Ala Asn			
500	505	510	

Arg	Thr	Pro	Met	Tyr	Met	Thr	Asp	Ser	Asn	Asp	Thr	Ile	Ser	Asn	Gly
515							520					525			
Thr	Asn	Ala	Asn	Thr	Phe	Ser	Leu	Asp	Leu	Lys	Thr	Ile	Leu	Val	Ser
530						535					540				
Thr	Ala	Met	Gly	Cys	Phe	Thr	Phe	Leu	Gly	Val	Val	Leu	Phe	Cys	Phe
545					550				555			560			
Leu	Leu	Leu	Phe	Val	Trp	Ser	Arg	Gly	Lys	Gly	Lys	His	Lys	Asn	Ser
							565		570			575			
Ile	Asp	Leu	Glu	Tyr	Val	Pro	Arg	Lys	Asn	Ser	Gly	Ala	Val	Val	Glu
							580		585			590			
Gly	Glu	Val	Ala	Gly	Pro	Arg	Arg	Phe	Asn	Met	Lys	Met	Ile		
							595		600			605			

<210> 19
 <211> 1215
 <212> DNA
 <213> Homo sapiens

<400> 19
 gctccttctc tccctctcca gaagtccatt ggaatattaa gcccaggagt tgctttgggg 60
 atggctggaa gtgcaatgtc ttccaagttc ttcctagtgg ctttggccat attttctcc 120
 ttgcggcagg ttgttaatgtc agccaattct tggtggtcgc taggttatgaa taaccctgtt 180
 cagatgtcag aagtatataat tataggagca cagcctcttgc gcaaggcaact ggcaggactt 240
 tctcaaggac agaagaact gtgccacttg tatcaggacc acatcgatca catcgagaa 300
 ggcgcgaaga caggcatcaa agaatgccag tatcaattcc gacatcgaaat gtggaaactgc 360
 agcaactgtgg ataacacctc tgggtttggc aggggtatgc agataggttag cccgcgacgc 420
 gccttcacat acgcggtgag cgccagcagggt gttggtaacgc ccatgagccg ggcgtgccc 480
 gagggcgagc tggccacctg cgctgcagc cgccggcgc gccccaaagga cctggccgg 540
 gactggctct gggcggtc cgccgcacc aacaaaaaaag gctaccgctc cgccaaaggag 600
 atcgtgcacg cccgcgaacgc aggacgcac tcaacgcacgg gctcctacga gagtgctcgc 660
 atcctcatga acctgcacaa caacgaggcc ggccgcaggat cgggttacaa cctggctgat 720
 gtggcctgca agtgcacatgg ggtgtccggc tcatgttagcc tgaagacatg ctggctgcag 780
 ctggcagact tccgcacatgg ggtgtatgcctt ctgaaggaga agtacgcacag cgccggcc 840
 atgcggctca acagccgggg caagttggta caggtaaca gccgccttcaa ctcgcccacc 900
 acacaagacc tggtctacat cgacccccagc cctgactact gcgtgcgcacaa tgagagcacc 960
 ggctcgctgg gcacgcaggcc cccgcgtgtgc aacaagacgt cggaggccat ggatggctgc 1020
 gagctcatgt gctgcggccg tgctacgcac cagttcaaga cctgtgcacgc ggagcgctgc 1080
 cactgcaagt tccactgggtc ctgctacgtc aagtgcacaa agtgcacggc gatcgtggac 1140
 cagttgtgt gcaagtatgt ggtgccaccc agcactcagc cccgcgtccca ggacccgctt 1200
 atttatagaa agtac 1215

<210> 20
 <211> 380
 <212> PRT
 <213> Homo sapiens

<400> 20
 Leu Gln Lys Ser Ile Gly Ile Leu Ser Pro Gly Val Ala Leu Gly Met
 1 5 10 15
 Ala Gly Ser Ala Met Ser Ser Lys Phe Phe Leu Val Ala Leu Ala Ile
 20 25 30
 Phe Phe Ser Phe Ala Gln Val Val Ile Glu Ala Asn Ser Trp Trp Ser
 35 40 45

Leu Gly Met Asn Asn Pro Val Gln Met Ser Glu Val Tyr Ile Ile Gly
 50 55 60

Ala Gln Pro Leu Cys Ser Gln Leu Ala Gly Leu Ser Gln Gly Gln Lys
 65 70 75 80

Lys Leu Cys His Leu Tyr Gln Asp His Met Gln Tyr Ile Gly Glu Gly
 85 90 95

Ala Lys Thr Gly Ile Lys Glu Cys Gln Tyr Gln Phe Arg His Arg Arg
 100 105 110

Trp Asn Cys Ser Thr Val Asp Asn Thr Ser Val Phe Gly Arg Val Met
 115 120 125

Gln Ile Gly Ser Arg Glu Thr Ala Phe Thr Tyr Ala Val Ser Ala Ala
 130 135 140

Gly Val Val Asn Ala Met Ser Arg Ala Cys Arg Glu Gly Glu Leu Ser
 145 150 155 160

Thr Cys Gly Cys Ser Arg Ala Ala Arg Pro Lys Asp Leu Pro Arg Asp
 165 170 175

Trp Leu Trp Gly Gly Ser Gly Ala Thr Asn Lys Lys Gly Tyr Arg Ser
 180 185 190

Ala Lys Glu Ile Val His Ala Arg Glu Arg Gly Arg Ile His Ala Lys
 195 200 205

Gly Ser Tyr Glu Ser Ala Arg Ile Leu Met Asn Leu His Asn Asn Glu
 210 215 220

Ala Gly Arg Arg Thr Val Tyr Asn Leu Ala Asp Val Ala Cys Lys Cys
 225 230 235 240

His Gly Val Ser Gly Ser Cys Ser Leu Lys Thr Cys Trp Leu Gln Leu
 245 250 255

Ala Asp Phe Arg Lys Val Gly Asp Ala Leu Lys Glu Lys Tyr Asp Ser
 260 265 270

Ala Ala Ala Met Arg Leu Asn Ser Arg Gly Lys Leu Val Gln Val Asn
 275 280 285

Ser Arg Phe Asn Ser Pro Thr Thr Gln Asp Leu Val Tyr Ile Asp Pro
 290 295 300

Ser Pro Asp Tyr Cys Val Arg Asn Glu Ser Thr Gly Ser Leu Gly Thr
 305 310 315 320

Gln Gly Arg Leu Cys Asn Lys Thr Ser Glu Gly Met Asp Gly Cys Glu
 325 330 335

Leu Met Cys Cys Gly Arg Gly Tyr Asp Gln Phe Lys Thr Val Gln Thr
 340 345 350

Glu Arg Cys His Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys Lys
 355 360 365

Lys Cys Thr Glu Ile Val Asp Gln Phe Val Cys Lys
 370 375 380

<210> 21
<211> 4113
<212> DNA
<213> Homo sapiens

<400> 21

attaattctg gctccacttg ttgctcgcc caggttggg agaggacgga gggttggccgc 60
agcggttcc tgagtgaatt acccaggagg gactgacac agcacaact agagagggt 120
caggggtgc gggactcgag cgagcaggaa ggaggcagcg cctggcacca gggctttgac 180
tcaacagaat tgagacacgt ttgtaatcg tggcgccgc cgcgcacagg atcccagcga 240
aaatcagatt tcctggtag gttgcgtggg tggataatt tgaaaaaaaga aactgcctat 300
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Gly Met Asn Asn Pro Val Gln Met Ser Glu Val Tyr Ile Ile Gly
 50 55 60
 Ala Gln Pro Leu Cys Ser Gln Leu Ala Gly Leu Ser Gln Gly Gln Lys
 65 70 75 80
 Lys Leu Cys His Leu Tyr Gln Asp His Met Gln Tyr Ile Gly Glu Gly
 85 90 95
 Ala Lys Thr Gly Ile Lys Glu Cys Gln Tyr Gln Phe Arg His Arg Arg
 100 105 110
 Trp Asn Cys Ser Thr Ala Asp Asn Thr Ser Val Phe Gly Arg Val Met
 115 120 125
 Gln Ile Gly Ser Arg Glu Thr Ala Phe Thr His Ala Val Ser Ala Ala
 130 135 140
 Gly Val Val Asn Ala Ile Ser Arg Ala Cys Arg Glu Gly Glu Leu Ser
 145 150 155 160
 Thr Cys Gly Cys Ser Arg Thr Ala Arg Pro Lys Asp Leu Pro Arg Asp
 165 170 175
 Trp Leu Trp Gly Gly Cys Gly Asp Asn Val Glu Tyr Gly Tyr Arg Phe
 180 185 190
 Ala Lys Glu Phe Val Asp Ala Arg Glu Arg Glu Lys Asn Phe Ala Lys
 195 200 205
 Gly Ser Glu Glu Gln Gly Arg Val Leu Met Asn Leu Gln Asn Asn Glu
 210 215 220
 Ala Gly Arg Arg Ala Val Tyr Lys Met Ala Asp Val Ala Cys Lys Cys
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260					265								270		
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275						280							285		
Ser	Arg	Phe	Asn	Ser	Pro	Thr	Thr	Gln	Asp	Leu	Val	Tyr	Ile	Asp	Pro
290					295							300			
Ser	Pro	Asp	Tyr	Cys	Val	Arg	Asn	Glu	Ser	Thr	Gly	Ser	Leu	Gly	Thr
305					310					315				320	
Gln	Gly	Arg	Leu	Cys	Asn	Lys	Thr	Ser	Glu	Gly	Met	Asp	Gly	Cys	Glu
325						330							335		
Leu	Met	Cys	Cys	Gly	Arg	Gly	Tyr	Asp	Gln	Phe	Lys	Thr	Val	Gln	Thr
340						345							350		
Glu	Arg	Cys	His	Cys	Lys	Phe	His	Trp	Cys	Cys	Tyr	Val	Lys	Cys	Lys
355						360							365		
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<210> 23
 <211> 1214
 <212> DNA
 <213> Homo sapiens

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Ser Leu Gly Met Asn Asn Pro Val Gln Met Ser Glu Val Tyr Ile Ile			
35	40	45	
Gly Ala Gln Pro Leu Cys Ser Gln Leu Ala Gly Leu Ser Gln Gly Gln			
50	55	60	
Lys Lys Leu Cys His Leu Tyr Gln Asp His Met Gln Tyr Ile Gly Glu			
65	70	75	80
Gly Ala Lys Thr Gly Ile Lys Glu Cys Gln Tyr Gln Phe Arg His Arg			
85	90	95	
Arg Trp Asn Cys Ser Thr Val Asp Asn Thr Ser Val Phe Gly Arg Val			
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Met Gln Ile Gly Ser Arg Glu Thr Ala Phe Thr Tyr Ala Val Ser Ala			
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Ala Gly Val Val Asn Ala Met Ser Arg Ala Cys Arg Glu Gly Glu Leu			
130	135	140	
Ser Thr Cys Gly Cys Ser Arg Ala Ala Arg Pro Lys Asp Leu Pro Arg			
145	150	155	160
Asp Trp Leu Trp Gly Gly Cys Gly Asp Asn Ile Asp Tyr Gly Tyr Arg			
165	170	175	
Phe Ala Lys Glu Phe Val Asp Ala Arg Glu Arg Glu Arg Ile His Ala			
180	185	190	
Lys Gly Ser Tyr Glu Ser Ala Arg Ile Leu Met Asn Leu His Asn Asn			
195	200	205	
Glu Ala Gly Arg Arg Thr Val Tyr Asn Leu Ala Asp Val Ala Cys Lys			
210	215	220	
Cys His Gly Val Ser Gly Ser Cys Ser Leu Lys Thr Cys Trp Leu Gln			
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Leu Ala Asp Phe Arg Lys Val Gly Asp Ala Leu Lys Glu Lys Tyr Asp			
245	250	255	
Ser Ala Ala Ala Met Arg Leu Asn Ser Arg Gly Lys Leu Val Gln Val			
260	265	270	
Asn Ser Arg Phe Asn Ser Pro Thr Thr Gln Asp Leu Val Tyr Ile Asp			
275	280	285	
Pro Ser Pro Asp Tyr Cys Val Arg Asn Glu Ser Thr Gly Ser Leu Gly			
290	295	300	
Thr Gln Gly Arg Leu Cys Asn Lys Thr Ser Glu Gly Met Asp Gly Cys			
305	310	315	320
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<210> 25

<211> 4213

<212> DNA

<213> Homo sapiens

<400> 25

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<210> 26
 <211> 1210
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> Wherein Xaa is any amino acid as defined in the specification

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 20 25 30

 Gly Lys Leu Ser Asp Tyr Gly Val Thr Val Pro Cys Ser Thr Asp Phe
 35 40 45

 Arg Gly Arg Phe Leu Ser His Val Val Ser Gly Pro Ala Ala Ala Ser
 50 55 60

 Ala Gly Ser Met Val Val Asp Thr Pro Pro Thr Leu Pro Arg His Ser
 65 70 75 80

 Ser His Leu Arg Val Ala Arg Ser Pro Leu His Pro Gly Gly Thr Leu
 85 90 95

 Trp Pro Gly Arg Val Gly Arg His Ser Leu Tyr Phe Asn Val Thr Val
 100 105 110

 Phe Gly Lys Glu Leu His Leu Arg Leu Arg Pro Asn Arg Arg Leu Val
 115 120 125

 Val Pro Gly Ser Ser Val Glu Trp Gln Glu Asp Phe Arg Glu Leu Phe
 130 135 140

 Arg Gln Pro Leu Arg Gln Glu Cys Val Tyr Thr Gly Gly Val Thr Gly
 145 150 155 160

 Met Pro Gly Ala Ala Val Ala Ile Ser Asn Cys Asp Gly Leu Cys Ala
 165 170 175

Gly Pro Ala Gly Leu Ile Arg Thr Asp Ser Thr Asp Phe Phe Ile Glu
 180 185 190
 Pro Leu Glu Arg Gly Gln Gln Glu Lys Glu Ala Ser Gly Arg Thr His
 195 200 205
 Val Val Tyr Arg Arg Glu Ala Val Gln Gln Asp Phe Gly Leu Gly Asp
 210 215 220
 Leu Pro Asn Leu Leu Gly Leu Val Gly Asp Gln Leu Gly Asp Thr Glu
 225 230 235 240
 Arg Lys Arg Arg His Ala Lys Pro Gly Ser Tyr Ser Ile Glu Val Leu
 245 250 255
 Leu Val Val Asp Asp Ser Val Val Arg Phe His Gly Lys Glu His Val
 260 265 270
 Gln Asn Tyr Val Leu Thr Leu Met Asn Ile Val Ser Val Asp Glu Ile
 275 280 285
 Tyr His Asp Glu Ser Leu Gly Val His Ile Asn Ile Ala Leu Val Arg
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 Leu Ile Met Val Gly Tyr Arg Gln Ser Leu Ser Leu Ile Glu Arg Gly
 305 310 315 320
 Asn Pro Ser Arg Ser Leu Glu Gln Val Cys Arg Trp Ala His Ser Gln
 325 330 335
 Gln Arg Gln Asp Pro Ser His Ala Glu His His Asp His Val Val Phe
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 Met Cys His Pro Leu Arg Ser Cys Ala Leu Asn His Glu Asp Gly Phe
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 485 490 495
 Lys Gln Leu Trp Cys Ser His Pro Asp Asn Pro Tyr Phe Cys Lys Thr
 500 505 510

Lys Lys Gly Pro Pro Leu Asp Gly Thr Glu Cys Ala Pro Gly Lys Trp
 515 520 525
 Cys Phe Lys Gly His Cys Ile Trp Lys Ser Pro Glu Gln Thr Tyr Gly
 530 535 540
 Gln Asp Gly Gly Trp Ser Ser Trp Thr Lys Phe Gly Ser Cys Ser Arg
 545 550 555 560
 Ser Cys Gly Gly Val Arg Ser Arg Ser Arg Ser Cys Asn Asn Pro
 565 570 575
 Ser Pro Ala Tyr Gly Arg Leu Cys Leu Gly Pro Met Phe Glu Tyr
 580 585 590
 Gln Val Cys Asn Ser Glu Glu Cys Pro Gly Thr Tyr Glu Asp Phe Arg
 595 600 605
 Ala Gln Gln Cys Ala Lys Arg Asn Ser Tyr Tyr Val His Gln Asn Ala
 610 615 620
 Lys His Ser Trp Val Pro Tyr Glu Pro Asp Asp Asp Ala Gln Lys Cys
 625 630 635 640
 Glu Leu Ile Cys Gln Ser Ala Asp Thr Gly Asp Val Val Phe Met Asn
 645 650 655
 Gln Val Val His Asp Gly Thr Arg Cys Ser Tyr Arg Asp Pro Tyr Ser
 660 665 670
 Val Cys Ala Arg Gly Glu Cys Val Pro Val Gly Cys Asp Lys Glu Val
 675 680 685
 Gly Ser Met Lys Ala Asp Asp Lys Cys Gly Val Cys Gly Gly Asp Asn
 690 695 700
 Ser His Cys Arg Thr Val Lys Gly Thr Leu Gly Lys Ala Ser Lys Gln
 705 710 715 720
 Ala Gly Ala Leu Lys Leu Val Gln Ile Pro Ala Gly Ala Arg His Ile
 725 730 735
 Gln Ile Glu Ala Leu Glu Lys Ser Pro His Arg Ile Val Val Lys Asn
 740 745 750
 Gln Val Thr Gly Ser Phe Ile Leu Asn Pro Lys Gly Lys Glu Ala Thr
 755 760 765
 Ser Arg Thr Phe Thr Ala Met Gly Leu Glu Trp Glu Asp Ala Val Glu
 770 775 780
 Asp Ala Lys Glu Ser Leu Lys Thr Ser Gly Pro Leu Pro Glu Ala Ile
 785 790 795 800
 Ala Ile Leu Ala Leu Pro Pro Thr Glu Gly Gly Pro Arg Ser Ser Leu
 805 810 815
 Ala Tyr Lys Tyr Val Ile His Glu Asp Leu Leu Pro Leu Ile Gly Ser
 820 825 830
 Asn Asn Val Leu Leu Glu Glu Met Asp Thr Tyr Glu Trp Ala Leu Lys
 835 840 845
 Ser Trp Ala Pro Cys Ser Lys Ala Cys Gly Gly Ile Gln Phe Thr

850	855	860													
Lys	Tyr	Gly	Cys	Arg	Arg	Arg	Arg	Asp	His	His	Met	Val	Gln	Arg	His
865				870					875					880	
Leu	Cys	Asp	His	Lys	Lys	Arg	Pro	Lys	Pro	Ile	Arg	Arg	Arg	Cys	Asn
				885				890					895		
Gln	His	Pro	Cys	Ser	Gln	Pro	Val	Trp	Val	Thr	Glu	Glu	Trp	Gly	Ala
				900				905					910		
Cys	Ser	Arg	Ser	Cys	Gly	Lys	Leu	Gly	Val	Gln	Thr	Arg	Gly	Ile	Gln
				915			920				925				
Cys	Leu	Leu	Pro	Leu	Ser	Asn	Gly	Thr	His	Lys	Val	Met	Pro	Ala	Lys
				930			935			940					
Ala	Cys	Ala	Gly	Asp	Arg	Pro	Glu	Ala	Arg	Arg	Pro	Cys	Leu	Arg	Val
				945			950			955			960		
Pro	Cys	Pro	Ala	Gln	Trp	Arg	Leu	Gly	Ala	Trp	Ser	Gln	Cys	Ser	Ala
				965			970					975			
Thr	Cys	Gly	Glu	Gly	Ile	Gln	Gln	Arg	Gln	Val	Val	Cys	Arg	Thr	Asn
				980			985					990			
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				995			1000			1005					
Val	Cys	Ser	Leu	Pro	Ala	Cys	Asn	Lys	Ile	Ser	Ser	Thr	Glu	Pro	Cys
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Thr	Gly	Asp	Arg	Ser	Val	Phe	Cys	Gln	Met	Glu	Val	Leu	Asp	Arg	Tyr
				1025			1030			1035			1040		
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				1060			1065			1070					
Pro	Pro	Phe	Ser	Thr	Pro	Gly	Ser	Pro	Leu	Pro	Gly	Pro	Gln	Asp	Pro
				1075			1080			1085					
Ala	Asp	Ala	Ala	Glu	Pro	Pro	Gly	Lys	Pro	Thr	Gly	Ser	Glu	Asp	His
				1090			1095			1100					
Gln	His	Gly	Arg	Ala	Thr	Gln	Leu	Pro	Gly	Ala	Leu	Asp	Thr	Ser	Ser
				1105			1110			1115			1120		
Pro	Gly	Thr	Gln	His	Pro	Phe	Ala	Pro	Glu	Thr	Pro	Ile	Pro	Gly	Ala
				1125			1130					1135			
Ser	Trp	Ser	Ile	Ser	Pro	Thr	Thr	Pro	Gly	Gly	Leu	Pro	Trp	Gly	Trp
				1140			1145					1150			
Thr	Gln	Thr	Pro	Thr	Pro	Val	Pro	Glu	Asp	Lys	Gly	Gln	Pro	Gly	Glu
				1155			1160			1165					
Asp	Leu	Arg	His	Pro	Gly	Thr	Ser	Leu	Pro	Ala	Ala	Ser	Pro	Val	Thr
				1170			1175			1180					
Xaa	Ala	Val	Pro	Cys	His	Pro	Thr	Gly	Thr	Phe	Thr	Leu	Cys	Val	Leu
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1205 1210

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<213> Homo sapiens

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aaagaaggat gatagggaca agaaaaaagaa atatgaacct cctataccag ctagagttag 120
gaagaagaag aaaacaaagg gaccagatgc tgccagcaaa ctgcccactga tgacacctca 180
caactctgtgc cagttaaaat tattgaaatt agagataatt aaatactgtc ttctcatgaa 240
ggaagaattc attagaaatc agaacaat gaaactatta gaaggaaagc aagaggagga 300
aagatcaaaa gtggatgatc tgagggggac ccccatgtca gtagtaacct tggaaagagat 360
tattgatgac aatcatgcca tcatagtctac atctgtggc ttagagcatc tgtggctca 420
gagcattctt gtagacaagg atctgtctgg acctgctgc tcggccctgc tcaaccacaa 480
ggttcgtgct gtgatatggg tgctgtatgg tgacacggat acccttagtca caatgatgaa 540
ggtggaaaag accccccagg agacctgtgt tgatactggg gggttggaca gccaaattca 600
ggaaattaag gaatttgtgg agttccctct cacacattct gaatattatg aagagatggg 660
tataaagccc cctaaggggag tcattacta tggtccaccc ggcacaggta aaaccttgg 720
agccaaagca gtagcaaacc acatcttagc cacttcttg caagtgtatca gctctgaatt 780
tattcagaaa tacctacatg atgggccccaa actcatatgg gaatttggc tagttgctga 840
agaacatgca cttccatca tggatttattga tggaaattgat gctatttaga caaaaagatg 900
tgactcaaattcgtataagtg agagagaaaat tcagcaaata atgctggaaa tggtaacca 960
gttggatgga ttgtattca ggggagatgt gaaaggatc atatccacaa gccgaataga 1020
aactttggat ctgcactta tcagaccagg ctacactgac aggaagctca agttccccct 1080
gcctgtgaa aagactaaga agcacatctt tcagatgcac acaaggcaggat ttacgctggc 1140
caatgatata atccctggaca actccatcat ggctaaatgat gacctctttt gtacagaccc 1200
caaggcaatc tgcacagaaat ctgtctgtat ggcctttttttaaa gaacatggaa tggaaatgaa 1260
aaatgaaaac ttcaaaaaat ctcagaaaaa tggattttttaaa aagaacagg aagacacccc 1320
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accagatatt 1390

<210> 28
<211> 452
<212> PRT
<213> Homo sapiens

<400> 28
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Asp Asp Arg Asp Lys Lys Lys Tyr Glu Pro Pro Ile Pro Ala Arg
20 25 30
Val Arg Lys Lys Lys Lys Thr Lys Gly Pro Asp Ala Ala Ser Lys Leu
35 40 45
Pro Leu Met Thr Pro His Thr Leu Cys Gln Leu Lys Leu Leu Lys Leu
50 55 60
Glu Ile Ile Lys Tyr Cys Leu Leu Met Lys Glu Glu Phe Ile Arg Asn
65 70 75 80
Gln Glu Gln Met Lys Leu Leu Glu Gly Lys Gln Glu Glu Glu Arg Ser
85 90 95
Lys Val Asp Asp Leu Arg Gly Thr Pro Met Ser Val Val Thr Leu Glu
100 105 110

Glu Ile Ile Asp Asp Asn His Ala Ile Met Ser Thr Ser Val Gly Ser
 115 120 125
 Glu His Leu Trp Ala Gln Ser Ile Leu Val Asp Lys Asp Leu Leu Glu
 130 135 140
 Pro Gly Cys Ser Val Leu Leu Asn His Lys Val Arg Ala Val Ile Trp
 145 150 155 160
 Val Leu Met Asp Asp Thr Asp Thr Leu Val Thr Met Met Lys Val Glu
 165 170 175
 Lys Thr Pro Gln Glu Thr Cys Val Asp Thr Gly Gly Leu Asp Ser Gln
 180 185 190
 Ile Gln Glu Ile Lys Glu Phe Val Glu Leu Pro Leu Thr His Ser Glu
 195 200 205
 Tyr Tyr Glu Glu Met Gly Ile Lys Pro Pro Lys Gly Val Ile His Tyr
 210 215 220
 Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys Ala Val Ala Asn
 225 230 235 240
 His Ile Leu Ala Thr Phe Leu Gln Val Ile Ser Ser Glu Phe Ile Gln
 245 250 255
 Lys Tyr Leu His Asp Gly Pro Lys Leu Ile Trp Glu Leu Phe Leu Val
 260 265 270
 Ala Glu Glu His Ala Pro Ser Ile Met Phe Ile Asp Glu Ile Asp Ala
 275 280 285
 Ile Arg Thr Lys Arg Cys Asp Ser Asn Ser Asp Ser Glu Arg Glu Ile
 290 295 300
 Gln Gln Ile Met Leu Glu Met Leu Asn Gln Leu Asp Gly Phe Asp Ser
 305 310 315 320
 Arg Gly Asp Val Lys Val Ile Ile Ser Thr Ser Arg Ile Glu Thr Leu
 325 330 335
 Asp Leu Ala Leu Ile Arg Pro Gly Tyr Thr Asp Arg Lys Leu Lys Phe
 340 345 350
 Pro Leu Pro Asp Glu Lys Thr Lys Lys His Ile Phe Gln Met His Thr
 355 360 365
 Ser Arg Ile Thr Leu Ala Asn Asp Thr Ile Leu Asp Asn Ser Ile Met
 370 375 380
 Ala Lys Asp Asp Leu Ser Cys Thr Asp Leu Lys Ala Ile Cys Thr Glu
 385 390 395 400
 Ala Ser Leu Met Ala Leu Lys Glu His Gly Met Lys Val Thr Asn Glu
 405 410 415
 Asn Phe Lys Lys Ser Gln Glu Asn Val Leu Tyr Lys Glu Gln Glu Asp
 420 425 430
 Thr Pro Lys Gly Leu Cys Leu Gly Ser Lys Arg Lys Lys Gly Lys Gly
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450

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<220>
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primers

<400> 29
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22

<210> 30
<211> 25
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<213> Artificial Sequence

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<400> 30
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25

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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primers

<400> 31
tgacaaggag cttactcttc ca

22

<210> 32
<211> 19
<212> DNA
<213> Artificial Sequence

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<400> 32
ccgttcactc ttgcaaagg

19

<210> 33
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gggccttac caactctgaa	20
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<400> 38
gacacctagat gtccttagcca at 22

<210> 39
<211> 26
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<220>
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<400> 39
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<210> 40
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<400> 40
ccagggaaaca ctcactcaca tt 22

<210> 41
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<400> 41
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<210> 42
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<400> 42
tcctgtctct catcctctac atttcacca 30

<210> 43
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<400> 43
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<210> 44
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<400> 44
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<210> 45
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<210> 46
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agggctccag agaagatgtc ta                                22

<210> 47
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<210> 48
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<210> 54
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<210> 55
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<212> DNA
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<210> 56
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<210> 57
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<210> 58
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<210> 59
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primers

<400> 59
ccaagttctt cctagtggtt tt 22

<210> 60
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primers

<400> 60
tttctcccttc gcccaggttg taattg 26

<210> 61
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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primers

<400> 61
ataccttagcg accaccaaga at 22